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SEQ ID NO: 6	A33	1	W Y G K W W P V L W T L C A V R V T Y D A I S V E T P Q D V L R A S S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1	40628	1	W G T K A Q V E R K L C F I L A I L C S L A L G S V T V H S S E P E V A I P E
SEQ ID NO: 2	45416	1	... W G I L L G L L L G H L T Y D I Y G R P I L E V P E S V T G P W K G D V N I L P C T Y D P L
SEQ ID NO: 9	35638	1	W A R R S R H R L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V V T A V E
SEQ ID NO: 10	JAM	1	W G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S O V Q P E
A33	51	S R E G L I Q W O K L L L T E R V V I W P F S H N K N Y I H G E L Y K N R V S I S H N A E Q S D A	
40628	43	N N P V K L S C A Y S G F S S P R V E W K F D Q G D T T R L Y C Y N N K I T A S Y E D R V T F L P T	
45416	47	Q G Y T Q V L Y K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G O V	
35638	43	Y Q E A I L A C K T P K X T Y S S R L E W K K L G R S Y S F Y Y Q Q T L Q G D F K H A E M I D F	
JAM	42	N E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L Y C Y N S Q I T A P Y A D R V T F S S S	
A33	101	S I T I D Q L T I A D N G T Y E C S V S L S D L E G N T K S V A Y R L V L V P P S K	
40628	93	G I T F K S V T R E D T G T Y T C H V S E E G G N S Y G E V K Y K L I V L V P P S K	
45416	97	S I Q L S T L E W D D O R S H Y T C E V T W O T P D G N O V V R D K I T E L R V Q K L S V S K P T V T	
35638	93	N I R I K N V T R S D A G K Y R C E V S A P S E O G Q N L E E D T Y T L E V L V A P V	
JAM	92	G I T F S S V T R K D N G E Y T C H V S E E G G Q H N Y G E V S I H L T V L V P P S K	
A33	144	P E C G I E G E T I I G N N I O L T C Q S K E G S P T P O Y S W K R Y N I L N Q E O	
40628	135	P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V W M P T N . P K S T R A F	
45416	147	T G S G Y G F T V P Q G M R I S L Q C Q A R . G S P P I S Y I W Y K Q Q T N N Q E P	
35638	137	P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R I L L E N . P R L G S Q S	
JAM	134	P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S W L T A D A K K T R A F	

FIG.-1A

SEQ ID NO: 6	A33	186	PLAQPASGGPVSSLKNISTOTS	GYCTSSNEEG.....TQFCNITV
SEQ ID NO: 1	40628	184	SNSSYLNPPTGELVFDPLSASD	TGEYSCEARNYG.....TPMTSNAY
SEQ ID NO: 2	45416	188	IKVATLSTLLFKPAVIADS	GSYFCTAKGAVGSEQHSDIVKFVVKD
SEQ ID NO: 9	35638	186	TNSSYTWNTKTGTLOFTVSKLDI	FDTGEYSCEARNSVG.....YRRCPGKR
SEQ ID NO: 10	JAM	184	WNSSFTIDPKSGDLIFDOPVTA	FDSEYYCDAQNYG.....IAHSEAKA
A33	227	AVRSPSWNVALLYGIAVGVVAA	LIIIGIIIIYCCCCRGKDDNTEDKEDA..	
40628	228	RMEAVERNYGYIVAAVLYTLILL	GILYFGIWFAYSRGHFDRTKKGTSS..	
45416	233	SSKLTKTEAPTTMITYPLKATSTV	KQSWDWTTDMDGYLGETISAGPGKS	
35638	230	MQVDDLNISGIIAAVYVVALVISV	CGLGVCYAQORKGYFSKEETSFAQKS..	
JAM	228	HMDAVELNVGGIVAAVVLVTLL	LLIFGVWFAYSRGYFETTKKGITAP..	
A33	275	RPNREAYEEPPPEQLREL	REEDDYRQEERQRSTGRESPDHLDO	
40628	275	...SKKVIYSOPSARSEGEFFKOTSS	FLV.....	
45416	283	PVFAILLISLCCMVVFTHAYIWL	CRKTSGOEHVYEAAAR.....	
35638	277	WSSSSKATTWSENVQWLTPVIPALW	KAAGGSRGQEF.....	
JAM	276GKKVIYSOPSARSEGEFFKOTSS	FLV.....	

FIG.-1B

SEQ ID NO:1

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe	Ile	Ile	Leu	Ala	Ile	Leu	Cys	Ser	Leu	Ala	Ile	Gly	Ser	Val	Thr	
1										10					15			20			25									10
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val	
									35						40			45			50									60
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Phe	Leu		
									65						70			75			80									90
Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	Val	Arg	Glu	Asp	Thr	Gly	Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	Gly	Gly	Asn	Ser	Tyr	Gly			
									95						100			105			110								115	120
Glu	Val	Lys	Val	Ile	Val	Leu	Val	Pro	Pro	Ser	Lys	Pro	Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	Thr	Ile	Gly	Asn	Ser	Tyr	Gly			
									125						130			135			140								145	150
Ileu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	Pro	Ser	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	Pro	Lys	Ser	Thr	
									155						160			165			170								175	180
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr	
									185						190			195			200								205	210
Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	Asn	Ala	Val	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Ile	Val			
									215						220			225			230								235	240
Ala	Ala	Val	Val	Thr	Leu	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe	Gly	Ile	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys		
									245						250			255			260								265	270
Lys	Gly	Thr	Ser	Ser	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	Arg	Ser	Glu	Gly	Glu	Phe	Lys	Gln	Thr	Ser	Ser	Phe	Leu	Vai		
									275						280			285			290								295	299

FIG._2

SEQ ID NO:2

1 **MGILIGLLL GHITVDTYGR FILEVPESVT GPKGDNLP CTYDPLQGYT QVLVKMLVQR GSDPVTFIFR DSSGDHICQA KYQGRLLHVSH KVPGDVSIQL**

101 **STLEMDDRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTGSG YCFTVPQGMR ISLQCQARGC PPISYIWYKQ QTNNQEPIKV ATLSLJLFKP**
 ~Glycosaminoglycan attachment site

201 **AVIADSGSYF CTAKGQVGSE QHSDIVKFVV KDSSKLKKTK TEAPTTMVTYP LKATSTVKQS WDWTTDMGY LGETSAGPK SLPVFAILLI ISLCCMVVF**
 ~Transmembrane domain

301 **MAYIMLCKT SQEHVYEAAR****FIG.-3**

OLI2162 (35936.f1)

SEQ ID NO:12

TCGGGGAGCTGTGTTCTGTGTTCCC

OLI2163 (35936.p1)

SEQ ID NO:13

TGATCGCGATGGGGACAAAGGCCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)

SEQ ID NO:14

ACACCTGGTTCAAAAGATGGG

OLI2165 (35936.r1)

SEQ ID NO:15

TAGGAAGAGTTGCTGAAGGCACGG

FIG.-8

DNA35936 SEQ ID NO:3

CTTCTTGC_{CA} ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
 GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
 GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
 CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
 AACAAAGATGG TTCCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
 GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
 TGTCCCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
 CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

FIG._4A

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
 CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
 GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150
 TGTGCTCCCT GGCATTGGC AGTGTACAG TTGCACTCTT CTGAACCTGA 200
 AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCTGT GCCTACTCGG 250
 GCTTTCTTC TCCCCGTGTG GAGTGGAAAGT TTGACCAAGG AGACACCACC 300
 AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
 GACCTTCTTG CCAACTGGTA TCACCTCAA GTCCGTGACA CGGGAAAGACA 400
 CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
 GAGGTCAAGG TCAAGCTCAT CGTGGTTGTG CCTCCATCCA AGCCTACAGT 500
 TAACATCCCC TCCTCTGCCA CCATTGGAA CCGGGCAGTG CTGACATGCT 550
 CAGAACAAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
 ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
 CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTGAT CCCCTGTCAG 700
 CCTCTGATAAC TGGAGAATAC AGCTGT 726

FIG._4B

consen02 SEQ ID NO:5

GCAGGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTGCCATC ATCCTCATCA TCTCCTTGTG 650
CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTGCCC TGGATTTCGC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTGGCATC TTGCCACCAAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTCCT CAGGGCCAGA CAGCTTTAA TTGAAATTGT 1400
TATTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503

FIG._4C

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SEQ ID NO:11 CGAGTCCTT CGGGGCTGT TGTGTCACTG GCCTCATGC GATGGGGACA AAGGGCAAG TCGAGGAA ACTGTGTGC CTCTTCATA 100
 TGGCAGATCCT GTTGTGCTCC CTGGCATTGG GCACTGTAC AGTCAACTCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT ATCCCTGTGA AGTGTGCTG 200
 TGCCTACTCG GGCTTTCTT CTCCCCGTGTT GGAGTGGAG TTGAGCCAAG GAGACACCAC CAGACTCGTT TGCTTAATA ACAAGATCAC AGCTTCCTAT 300
 GAGGACCCGGG TGACCTTCTT GCCAACTGGT ATCACCTCA AGTCCGTGAC ACAGGGACAT ACTGGGACAT ACACCTGTAT GGTCTGTAG GAAGGGGGCA 400
 ACAGCTATGG CGAGGTCAAAG GTCAAGCTCA TCGAGTCAAAG TTAAACATCCC AGGCTCATAG TTAAACATGCC ACCATGGGA ACCGGGGAGT 500
 GCTGACATGC TCGAGAACAG ATGGTCCCCC ACCTTCTGAA TACACCTGGT TCAAAAGATGG GATAGTGATG CCTACGAATC CCAAAGCAC CGGTGCTTC 600
 AGCAACTCTT CCTATGTCCT GAATCCACAA ACAGGAGGCC TGGTCTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGGTGTAG GCACGGAAATG 700
 GGTATGGAC ACCCATGACT TCAAATGCTG TGGCCTGGAA AGCCTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800
 GGGAAATCTG GTTTGGCA TCTGGTTGC CTAGCGGA GGCCACTTG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT 900
 AGTGCCTGAA GTGAAGGAGA ATTCAACAG ACCTCGTCAAT TCCCTGGTGC AGCCTGGTG GGTCAACGGCC TATCATCTGC ATTTGCTTA CTCAGGTGCT 1000
 ACCGGACTCT GGCCCCCTGAT GTCTGTAGTT TCAAGGATG CCTTATTGT CTCTACACC CCACAGGGCC CCTACTCTT TCGGATGTGT TTAAATAT 1100
 GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAACCT TGTAAAGT GTTATTCCC CATTCTCTG 1200
 AGGGATCAGG AGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAAA TGGGGGGT CGCAGGAATC TGCACTCAAC TGCCCACCTG 1300
 GCTGGCAGGG ATCTTGTAAAT AGCTATCTTG AGCTGGTTC TGGCCTCTT CCTGTGTAC TGACGACCG AGCCAGCTGT TCTAGGGCGG GAATTAGGG 1400
 CTAGAGGGCC TGAAATGGTT GTTGGTGT GACACTGGG TCCTTCATC TCTGGGGCC ACTCTCTCT GTCTTCCAT GGGAAAGTGCC ACTGGGATCC 1500
 CTCTGCTG TTCTCCTGAA TACAAGCTGA CTGACATGA CTGTGTGTGTT AGCTCTGT GTGGAGGAA TAGTAATTT TCAGAGAATCT 1600
 TGAAGCCAAA AGGATTAAA ACCGCTGCTC TAAAGAAAG AAAACTGGAG GCTGGCTCAGG CCTGTAATCC CAGGCTGA GGAGGGCGA 1700
 TCACCTGAGG TCGGGAGTTC GGGATCAGCC TGACCAACAT GGAGAACCC TACTGGAAAT ACAAGTGTAG CGAGGCTATGC TGGTGTAGTCCC 1800
 AGCTGCTAG GAGGCTGGCA ACAAGGAGCAA AACTCCAGCT CA 1842

FIG._5

SEQ ID NO:7

1 CCCCCCCCTC CGCCCAACGGG TCCGCCAACG GGTCGGGCGA CCCGTCCGGG CCACAGAGG TTGAGCCTC TTGGTAGCA GGAGGCTGGA AGAAAGGACA
GGTGGCAG CCGGGTCCC AGGGGCTGC CCAGGGGGT GGGAGGGCC GGTGGTCTC AACCTGGAG AAACCATCGT CCTCCGACTT TCTTCCCTGT

101 GAAGTAGCTC TGGGTGTGAT GGGGATCTTA CTGGGCTCTGC TACTCCTGGG GCACCTAACAA GTGGACACTT ATGGGGTCC CATTCTGGAA GTGCCAGAGA
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGAGG ATGAGGACCC CGTGATTGT CACCTGTGAA TACCCGGAGG GTAGGACCTT CACGGTCTCT
1 SEQ ID NO:2 M G I L L G L L G H L T V D T Y G R P I L E V P E S
*MET

201 CTGTAACAGG ACCTTGGAAA GGGGATGCGA ATCTTCCCTG CACCTATGAC CCCCTGCCAG GCTACACCCA AGTCTTGTGAG AACTCTGCTG TACAACGTC
CACATTGTCC TCGAACCTTT CCCCTACTT TAGAAGGGAC GTGGATACTG GGGGACGTT TCAGAACCCAC TTGACCGACC ATGTTGGCACC
29 V T G P W K C D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAGACCCCT GTCACCATCTT TTCTTACGTGA CTCTTCTGGA GACCATATCC ACCAGGAAA GTACAGGCAA CGTACGGGC CGCCCTCATG TGACCCACAA GGTTCCACCA
GAGTCTGGGA CAGTGGTICA AACATGGACT GAGAAGACCT CTGGCTATAGG TCCTCCGGTT CATGGCTCCG GGGGACGTPAC ACTCTGGTCTT CCAAGGTCT
62 S D P V T I F L R D S S C D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGATATCCC TCCAATTGGAG CACCCCTGGAG ATGGATGACC GGACCCACTA CACGGTGAAG GTCACCTGGC AGACTCTGAA TGCCACCCAA GTCTGTGACAG
CTACATAGGG AGGTTAACCTC GTGGGACCTC TACCTACTGC CCTCTGGTGT GTCACACTT CAGTGGACCC TCTGAGGACT ACCGTTGGTT CAGGACTCTC
95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

201 ATAAGATTAC TCGGCTGGAAC TCTCTGTCTC CAAGCCCACA GTGACAACTG GCAGGGTTA TGGCTTCACTG GTGGCCCCAGG GAATGAGGAT
TATTCTAATG ACTCGAGGCA CAGGTCTTG AGAGACAGAG GTTCGGGTGT CACTGTTGAC CTCGGGGTCC CACGGAACTCC CTTACTCTA
129 K I T E L R V Q K L S V S K P T V T T G S G Y G F T V P Q V G M R I

501 TAGCCTCAA TGGCAGGCTC GGGCTCTCC TCCCCTACTG TATATTGGT ATAACCAACA GACTAATAAAC CACCAAACTC TCAAAACTG AACCCCTAAGT
ATCGGAAGTT ACGGTCTGGAG CCCCAAGAG AGGGTAGTCA ATATAAACCA TATTCTGGGT CTGATTATG GTCTGGATCG TTGGGATCA
162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

FIG.-6A

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SEQ ID NO:7 701 ACCTTACTCT TCAAGCCCGG CGTGATGCC GACTCACCC CCACTTCTG CACTGCCAAG GCGAACGGTC CCTCTGACCA GCACACCCGAC ATCTGAACT
 TGGAAATGAGA AGTTCGGAGC CCACTATCGG CTGAGTCGGG GGATAAAGAC GTGACGGTTCC CGGCTCCAAC CGAGACTCTGT CGTGTGGCTG TAACACTTCA
 SEQ ID NO:2 195 T L F K P A V I A D S G S Y F C T A K C Q V G S E Q H S D I V K F

801 TTGTGCTCAA AGACTCTCAA AGACCAAGAC TCAGGCCACCT ACAACCATGA CATACCCCTT GAAAGCAACA TCTACAGTGA AGCAGTCCTG
 AACCCAGTT TCTGAGGAGT TTGGATGACT TCTGGTACTG ACTCCGTTCTG TGTTGGTAA CTATGGGAA CTTTCGTTGT AGATGTCACT TCGTCAGGAC
 229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 GGACTGGACC ACTCACATGG ATGGCTTACCT TGGAGACGCC AGTCCCTGGGC CAGGAAAGAC CCTCCCTGTC TTTGCCATCA TCCTCATCAT CTCCCTTGTCC
 CCTGACCTGG TGACTGTACCC TACCGATGCA ACCTCTCTGG TCAACGCCCG GTCCCTTCTC GGACGGACAG AACCCGTTGT AGGAGTAGTA GAGGAACACG
 262 D W T T D M D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGTATGGTCC TTTTACAT GGCCTATATC ATGCCCTCTGTC CGAACAGAC CATCTCTACG AACAGGCCAG CTAGAAACT CTCTCTCTT
 ACATACACC AAAATGGTA CGGGATATAG TACGGAGAC CGCTTCTCTAG CCTTGTCTC GTACAGATGC TTGCTGGTC CATTCTTCA GAGGAGAAA
 295 C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTGTA CCCCGTCCCT GCCCCTCAATT TTGATTAATG CGAGGAANT TGCAAGAACG GCGCTGTCC ACAGACCCAA TCCTAAGGGC GGAGGGCTTC
 GGTAAAAACT GGGCCAGGA CGGGAGTTAA AACTAATGAC CGTCCTTTAC ACCTCCTTCC CCCACACCC TGTCTGGTT AGGATTCGG CCTCCGGAG

1201 AGGGTCAAGGA CATAGCTGCC TTCCCTCTCT CAGGCCACCTT CTGAGGTTGT TTGGCCCTC TGACACAAA CGATAATTAA GATCCATCTG CCTCTCTGCTT
 TCCCAGTCTT GTATGGACGG AAGGGAGAGA GTCCGGGAA GACTCCAACA AAACCCGGAG ACTTGTGTT CCTATTAAAT CTAGGTAGAC GGAAGACGAA

1301 CCAGAATCCC TGGGGCTCT GATCCCTGATA ATTAAATGGC AAGMATTGAG GGAGMAGGT GGGAAACAG GACCAAGGCC CCAAGTCCCT TCTTATGGGT
 GGTCTTGGG ACCCACCATC TAGGACTAT TAATTAACCG TTCTTAACTC CGTCTTCCA CCCTTGGTC TCCCACCCGT AGAATACCCA

1401 GGTCGGCTCT TGGGCCATAG CGCACATGCC AGAGAGGCC ACACACTCTGG AGAAAACCTG AGGGGGCCA TCTTCCGAG TGGCTCCCTC AGTCATGAGC
 CCACCGGAGA ACCCGGTATC CGGTGTACCC TCTCTCCCGT TCCTGAGACC TCTTGGTAC TCCCACCCGT AGAAGGGT ACACGGAGG TCACTACTCG

1501 CAACTCCCCA GAATCTGGCC AACAACTACT CTGATGAGCC CTGCACTAGGA CAGGACTTAC AGATCATGCC CCAGATCAAT GGCAACTACG CCCGGCTGGCT
 GTGAAAGGT CTAGACCCG TTGTGTGATGA GACTACTCGG TCTAGTACTTA CGGTATGTC CCCTTGTAGGC GGTCTAGTA CGGTATGTC CCGGGGGACGA

FIG._6B

SEQ ID NO:7

1601 GGACACAGT CCTCTGGATT ATGAGTTCTT CCCCACTGAG GGCAAAAGTG TCTGTTAAA ATGCCCAT AGCCAGGAT CTGCTGACAT AATTGCCTAG
CCTGTGTCAA CGACACTAA TACTAAACA CCCGTCATC CCGTTTAC AGACAAATTG TACGGGTTAA TCCGGTCTA GACGACTGTA TAAACGGATC

1701 TCAGTCCCTG CCTCTGGCAT GGCCCTCTTC CCTGCTTACCT CTCTTCCCTG ATAGCCCCAA GTGTCGGCCCT ACCAACACTG GACCCGCTGG GAGTCACCTGG
AGTCAGAAC CGAACGACTA CGCGAACGAG GCAAGATGGA GAGAAGGACCC TATCGGTTT CACAGGGGA TGCTGTGAC CTCGGGACC CTCACTGACC

1801 CTTGGCCCTG GAATTGGCCA GATCCCATCTC AACTAAGCCA GCTGGCTGGAT TTGGCTCTGG CCCCTCTAG TATCTCTGCC GGGGGCTTCTT GGTAACCTCTC
GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCAATTGGT CGACGGACTA AACCGAGACC CGGAAGACAT ATAGAGACGG CCCCGGAAGA CCATGAGGAG

1901 TCTAAATACC AGAGGGAAGA TCCCCATAGC ACTAGGACTT GGTCACTATG CCTACAGACA CTATTCAACT TTGGCATCTT GCCACCAAGA GACCCGAGG
AGATTATGG TCTCCCTCTT ACGGCTATCG TGATCTTGAA CCAGTAGTAC CGATGTCTGT GATAAGTTGA AACCGTAGAA CGGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGCT CGGCCAGCTC AGAGGACCAAG CTATATCCAG GATCATTTCT CTTCTTCAG GCCCAGACAG CTTTTAATTG AATTCTTAT TTACAGGGCC
TCCGAGTCGA GACGGTGGAG TCTCCTGGTC GATATGGTC CTAGTAAGA GAANGAGTC CGGTCTGTC GAAATTAAC TTAAACATA AAGTGTCCGG

2101 AGGGTTCACT TCTGGCTCCTC CACTATAAGT CTATGTTCTT GACTCTCTCC TGGTGGCTAA TAATATCTA ATCATMACAG C
TCCCAACTCA AGACGGAGGAC GTGATTTCA GATTACAGA CTGAGAGGG ACCACGGAGTT ATTATAGTT TACTATTCG C

FIG.-6C

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCT
 CAGAGCAGCCGGCTGCCGCCCGGGAAAGATGGCGAGCAGGAGGCCACCGCCTCCTCCT
 GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGC
 CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGGCTATTTAGCCTGCAA
 AACCCCAAAGAAGACTGTTCCCTCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTC
 CTTGTCTACTATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGA
 TTTCAATATCCGGATCAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGT
 TAGTGCCTCATCTGAGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
 AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGT
 AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATAACACATGGTTAACGGA
 TGGCATCCGTTGCTAGAAAATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACAC
 AATGAATACAAAAACTGGAACTCTGCAATTAAACTGTTCAAAACTGGACACTGGAGA
 ATATTCCCTGTGAAGGCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGAAACGAATGCA
 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGGCCTTAGTGAT
 TTCCGTTGTGGCCTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTCAAAAGAAC
 CTCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAGTAAAATGTGAGTG
 GCTCACGCCTGTAATCCCAGCACTTGGAAAGGCCGGCGGGCGGATCACGAGGTAGGA
 GTTCTAGACCAGTCTGCCAATATGGTGAACCCCCATCTACTAAAATACAAAAATTAG
 CTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTGGGAGACAGGAGAACACTTG
 ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGTAA
 CAGAGCAAGATTCCATCTAAAAATAAAATAAAATAAAATAACTGGTTTACCTG
 TGTAGAATTCTTACAATAATAGCTTGTATATTC

FIG._7

SEQ ID NO:9

MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKDQOVVTAVEYQEAILACKTPKKT
 LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN
 LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD
 GIRLLENPR
 LGSQSTNSTSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRM
 QVDDLNISGI
 IAAVVVVALVISVCGLGVCYAQRKGYFSKETS
 FQKSNSSSKATTMSENVQWLTPVIPALW
 KAAAGGSRGQEF

FIG._11

SEQ ID NO:5

1 CAGGCAAG TACCCGGCC CCCTCCATCT GACCCACAG CTTCCACAG ATGTATCCCT CCAATTGAGC ACCCTGGGC TGGATGACCGA GACCCACTAC
 CGTCGGTTC ATGGTCCCCG CGGACGTACA CTGGGTCTC CAAGCTCTC TACATAGGA CGTTAUCCTCG TGGACCTCT ACCTACTGGC CTCGGTGATC
 ^42257. f1 SEQ ID NO:18 ^42257. p1 SEQ ID NO:22

101 ACGTGTGAG TCACCTGGCA GACTCTGTAT GGCAACCAAG TCCTGAGACA TAAGTATTACT GAGCTCGTG TCCAGAAACT CTCTGCTCC AAACCCACAG
 TGCACACTC ACTGGACCTC CTGAGGGACTA CCGGTTTC AGGACTCTCT ATTCTTAATGA CTGGCTTCAAT AGGCTTCAAC AGGCTTGA GAGCACAGG TTGGGTGTC

201 TGACAACTGC CAGGGTTAT GGCTTCACGG TGGCCCGAGG ATAGGAGTT AGCCTTCAAT GCCAGGCTTC CGGCTTCTCC TCCCACATG TATATTGCT
 ACTGGTACCC GTGCCACATA CGGAAGTGGCC ACGGGTCCC TTACTCCTAA TCGGAAGTTA CGGCTCCAAG CCCAACAGG AGGGTAGCTCA ATATTAACCA

301 ATAAGCAACA GACTAAACAC CAGGGAAACCC ATCAAAGTAG CAACCTTAAG TACCTTACTC TTCAAGCCTG CGGTGATACC CGACTCAGGC TCCTTATTCT
 TATTGGTCTCTG CTGATTATTG GTCCCCCTGGG TAGTTTCATC GTTGGGATTC ATGGAATGAG AAGTCCGAC CCCACTATCG GCTGACTTCG AGGATAAAGA

401 GCACTGCCAA GGGCCAGGT GGCTCTGAG ACCACACCGA CATTGCAAG TTGTTGCTCA AAGACTCCTC AAAAGTCAACTC AAGACCAAGA CTGAGGGCACC
 CGTGACGGTT CCCGGTCCAA CGGAGACTTC CTGACTCTC AACCAAGCTT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCCTGG
 ^42257. r1 SEQ ID NO:20

501 TACAAACATG ACATACCCCT TGAAGGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CACTCCCTGG
 ATGTTGGTAC TGTATGGGA ACCTTCGTTG TAGATGTCAC TTGTCAGGA CCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACGGACCC

601 CCAGGAAGA GCCTGGCTGT CTGGCCATC ATCCTCATCA TCTCTTGTG CTGCTATGCTG GTGGCTTACCA TGGCCTATAT CATGGCTCTGT CGGAACACAT
 GCTCTTCTCT CGGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAAC AAAAATGGT ACCGGATATA GTACGAGACA GCCTCTGTA
 ^42257. f2 SEQ ID NO:19

701 CCCACAGA GCATGCTAC GAAGCAGCCA GGGCACATGC CAGAGGGCC AACGACTCTG GACAAACCAT GAGGGTGGCC ATCTTCGCA GTGGCTGCTC
 CGGTGTTCTT CGTACAGTG CTGGCTGGT CCCGGTACCG GTCTCTCCGG TTGGCTGAGAC CTCTTGGTA CTCCCCACGG TAGAAGGGTT CACCGACGAG

FIG._ 9A

SEQ ID NO:5

801 CAGTGTGAG CCACTTCCC AGAATCTGGG CCACAACTA CTCTGTGAG CCTCGATAG GACAGGAGTA CCAGATCATC GCCAGATCA ATGGCAACTA
GTCACACTC GGTGAAAGG TCTTAGACCC CGTGTGAT GAGACTACTC CGGACTATC CTGTCCTCAT GGTCTAGTAG CGGCTCTAGT TACCGGTGTGAT

901 CGCCCCCTG CTGGCACACAG TTCCCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGCTGTTAA AAATCCCCA TTAGGCCAGG ATCTGCTGAC
GGGGGGGAC GACCTGTGTC AAGGAGACCT AATACTCAA GACCGGTGAC TCCGGTTTC AGACAAATT TTACGGGT ATCTGGTCC TAGACGACTG

1001 ATAATGCCCT AGTCAGTCCCT TGCCCTCTGC ATGGCCCTTCT CTCCTGCTAC CTCTCTCCCT GGATAGCCCA AAGTCTCCGC CTACCAACAC TGAGGCCGCT
TATTACCGA TCAGTCAGGA ACGGAAAGACG TACCGGAAGA AGGGACGATG GAGAGAAGGA CCTATCGGGT TTACACGGG GATGGGTCTG ACCTGGCGA

1101 GGGACTCACT GCGCTTGCCC TCGAATTTC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTGGCTCT AGTATCTCTG GGGCCCTCT AGTATCTCTG CCGGGGGCTT
CCCTCACTGA CGAAAACGG ACCTTAACG GTCTACGTAG AGTCATTCG GTCCGCGACC TAAACCGACA CCCGGAAAGA TCATAGAGAC GGGCCCCGAA
~42257.f2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGAA GATGCCATA GCACTAGGAC TTGGTCTCATCA TCCCTACAGA CACTATTCA CTTGGCATC TTGGCACCAG
GACCATGAGG AGACATTAT GGTCTCCCT CTACGGGTAT CGTGATCTG AACCCTACT ACCGATGTCT GTGATAAGTT GAAACCGTAG AACGGTTGTC

1301 AAGACCCGAG GGGAGGCTCA CCTCTGCCAG CTCAGAGGAC CAGCTATAC CAGGATCATC TCTCTTCFT CAGGGCAGA CAGCTTTAA TTGAAATTG
TTCTGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCGATATAAG GTGCCGGTCT GTGAAATT AACTTAACCA

1401 TATTCACAG CCCAGGGTTC AGTTCTGCTC CTCACATCA AGCTTAATCT TCTGACTCTC TCTCTGTGCT CAATAATCTA CTAATCTAA CAGCAAAAAA
ATAAAGTGTGTC CGGTCCCAAG TCAAGACCGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCAAGA GTTATTATA GATTAGTATT GTCGTTTTTT

1501 AAA
TTT

FIG.- 9B

		FRAME	SCORE	MATCH	PCT
A33_HUMAN	A33 ANTIGEN PRECURSOR - HOMO SAPIENS	+1	246	81	30

A33_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIENNPKLSCAYSGFSSPR---VEW-KFDQGDTTRLWC--YNN
SEQ ID NO:23

A33_human 17 VTVDAISVETPQDVLRASQGKSVTLPCYYHTSTSSREGLIQWDKLLLTHTERVVIWPFSN
SEQ ID NO:24

DNA40628 283 K--ITAS-YEDRVTFL-----PTGITFKSVTREDTGTYTCMVS---BEGGNSYGEVKVK
A33_human 77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRRVR

DNA40628 427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIIVMPTNPKSTRAFSN
A33_human 135 LLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNINLQEQP-----

DNA40628 607 SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGGYTPMTSNAVRMEAVERNVGV---IVA
A33_human 187 ---LAQPASGQPVSILKN1STDTSGYYICTSSNEEGTQFCNCNITVAVRSPSMNTVALYVGIAV

DNA40628 775 AVLVTLLGILVFGIWFAYSRGHFDRT--KKGTSSKKVYISQP
A33_human 244 GVVAAIIIGIIY---CCCCRGKDDNTEDKEDARPNEAYEEP

FIG.- 10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19
 IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

DNA40628	112	LCSL--ALGSVTVSSEPEVRIPENNPKLSCAYSGFSSPR---V рЕW-KFDQGDТTRLVC
SEQ ID NO:25		* * * . . * . * * * * . * . * . * . * . * . * . * . *
A33 human	12	LCAVRTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSREGLIQWDKLILLTHTERVV
SEQ ID NO:26		

DNA40628	274	--YNNK--ITAS-YEDRVTFL-----PTGITFKSVTREDTGTYTCMVSEEGGNSYGEVK
		* . * * * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	72	WPFSNKNYIHGELYKRNRSVISNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628	421	--VKLLVLVPPSKPTVNIPSSATIGNRAVLTСSEQDGSPSPPSEYTWFKDGIУMPTNPKSTR
		* . * . * * * * * . * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	131	SRVRLLVLPVPSKPECIGIEGETIIGNNIQLTCOSKEGSPTPQYSWKRYNILNQEQP----

DNA40628	595	AFSNSSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV--
		* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	187	-LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALLYV

DNA40628	766	-IVAAVLVTLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIVYSQP
		* . * . * * . * * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	240	GIAVGVVAALLIIGIIY---CCCCRГKDDNNTEDKEDARPНREAYEEP

FIG.- 10B

SEQIDNO: 6 A33_hum 1 M V G K M W P V L W T L C A V R V T V D A I S V E T P O O V L R A S Q G K S V T L
 SEQIDNO: 1 40628 1 M G T K A Q V E R K L L C I L F I L A I L L C S . . L A L G S V T V H S S E P E V R I P E N N P V K L

A33_hum 42 P C T Y H T S T S R E G L I O W D K L L T H T E R V Y I W P P F S N K N Y I H G E L Y K N A V S I
 40628 49 S C A Y S G F S S P R . . V E W . K F D Q G D T T R L Y C . . Y N N K . . I T A S . Y E D R V T F

A33_hum 92 S N N A E Q S D A S I T I D O L T M A D N G T Y E C S V S L W M S D L E G N T K S R V A R L L V L V P P
 40628 90 L P T G I T F K S V T R E O T G T Y T C M V S E E G G . N S Y G E V K V K L I L V L V P P

A33_hum 142 S K P E C G I E G E T I I G N N I Q I L T C O S K E G S P T P Q Y S W K R Y N I L N O E O P
 40628 133 S K P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I U V M P T N P K S T R A

A33_hum 187 L A Q P A S G Q P V S L K N I S T D T S G Y I C T S S N E E G T Q F C N I T V A V R S
 40628 183 F S N S S Y V L N P T T G E . L V F D P L S A S D T G E Y S C E A R N G Y G T P W T S N A V R W E A

A33_hum 231 P S M N V A L Y V G I A V G V V A A L I I G I I I Y C C . C C R G K D D N T E D K E D A R P N R E
 40628 232 V E R N V G V . . . I V A A V L V T L I L G I L V F G I W F A Y S R G H F D A T K K G T S S K V

A33_hum 280 A Y E E P P E Q L R E L S R E R E E D D Y R Q E E Q R S T G R E S P D H L D Q
 40628 279 I Y S O P S A R S E G E F K O T S S F L V

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SEQ ID NO: 6 A33_hum 1 M V G K M W P V [WTLCAVRVTVDAISVETPAOVLRASSAGKS] V T L P C T Y H T S T S
 SEQ ID NO: 2 45416 1 . M G I L L G L L L G H L T V D T Y G R P I L E V P E S Y T G P W K G . D V N L P C T Y D P L Q G

A33_hum 51 S R E G L I Q W D K [L L T H T E R V V] I W . P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D
 45416 49 Y T Q V L V K W . . L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V . P G D

A33_hum 100 A S I T I D Q L T M A D N G T Y E C S Y S : L W S D L E G N T K S R V R L L V L V P P S
 45416 96 V S L Q A L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R V Q K L S V S K P T V

A33_hum 143 K P E C G I E G E T I I G N N I Q L T C O S K E G S P T P Q Y S W K R Y N I L N O E Q P L A O P A S
 45416 146 T T G S G Y G F T V P Q G W R I S L O C A A R . G S P P I S Y - W . . Y K Q Q T N N Q E P I K V A T

A33_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T . Q F C N I . T V A V Y R S P S W N V A L Y V G
 45416 193 L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F V V Y K D S S K L L K T K T E

A33_hum 241 I A V G V V A A [I I G I I I Y C C C C A R G K D] D N T E D K E D A R P N R E A Y E E P P E Q L R E
 45416 243 A P T T W T Y P L K A T S T V K Q S W D W T T D W D G Y L G E T S A G P G K S L P V F A I I I S

A33_hum 291 L S R E R E E E D D Y R O E E Q R S T G R E S P D H L D Q
 45416 293 L C C W V V F T M A Y I H L C R K T S Q Q E H V Y E A R

FIG.- 13

SEQ ID NO: 6	A33_hum	1 . . . M V G K W W P V L W T L C A V R Y T V D A I S V E T P O D V L R A S Q G K S V T L P C
SEQ ID NO: 9	35638	1 M A R R S R H R L L L L R Y L V V A L G Y H K A Y G F S A P K D O o a y v t a v e y o e a i l a c
A33_hum	44	T Y H T S T S S R E G L I Q W D K I L L T H T E R V Y I W P F S N K N Y I H G E L Y K N R V S I S N
35638	51 . . .	K T P K K T V S S R L E W K K L G R S Y S F V Y Y Q Q T . L Q G D . F K N R
A33_hum	94	N A E Q S D A S I T I D Q L T H A D N G T Y E C S Y S L M S D L E G N . T K S A V R L L V L V P P S
35638	87 . A E N I D F N I R I K N Y I R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A	
A33_hum	143	K P E C G I E G E T I I G N N I Q L T C E G S P T P Q Y S W K A Y N I L N Q E Q P L A Q P A S
35638	136	V P S C E V P S S A L S G T V V E L R C Q D E G N P A P E Y T W F K D G I A L L E N P R L G S O S
A33_hum	193	G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N I T V A V . . . R S P S M N V A L Y V
35638	186	T N S S Y T M N T K T G T L Q F N T . V S K L D T G E Y S C E A R N S V G Y R A C P G K R M Q V D D
A33_hum	240	G I A V G V V A A L I I G I I I Y C C . . . C C R A G K D D N T E D K E D A R P N R E A Y E E P P E
35638	235	L N I S G I I A A V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T
A33_hum	287	Q L R E L S A . E R E E E D D Y R Q E E Q R S T G R A E S P D H L D Q
35638	285	M S E N V Q W L T P V I P A L W K A A A G G S R G Q E F

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FIG.- 14

SEQ ID NO: 10 jam 1 **W G T E G K A G R K L L F L F T - S M W I L C S L V A G K G S V Y T A Q S D V Q V P E N E S I K L T C**
 SEQ ID NO: 1 40628 1 **W G T X A Q V E R K L L C F I L A I L L C S L A L G S V T Y H S S E P E V R I P E N N P V K L S C**

jam 50 **T Y S G F S S P R A V E W X F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S S V T**
 40628 51 **A Y S G F S S P R A V E W X F D Q G D T T R I L V C Y N N K I T A S Y E D D R V T F L P T G I T F K S V T**

jam 100 **R K D N C G E Y T C H V S E E G G O N Y G E V S I H L I T V L V P P S K P T I S V P S S V T I G N R A V**
 40628 101 **R E D T G I Y T C H V S E E G G N S Y G E V K Y K L I I V L V P P S K P T V N I P S S A T I G N R A V**

jam 150 **L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F W N S S F T I D P K S G O L I F**
 40628 151 **L T C S E A D G S P P S E Y T W F K D G I . V M P T N P K S T R A F S N S S Y V L N P T T G E L V F**

jam 200 **D P V T A F D S G E Y Y C O A O N G Y G T A M A R S E A A H M D A V E L N V G G I V A A V L V T L I L**
 40628 200 **D P L S A S D T G E Y S C E A R N G Y G T P M T S N A V R M E A V E R N V G G I V A A V L V T L I L**

jam 250 **L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R A S E G E F K Q T S S F L**
 40628 250 **L G I L V F G I W F A Y S R G H F D R T K K G T . S S K K V I Y S Q P S A R S E G E F K Q T S S F L**

jam 300 **V**
 40628 299 **V**

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L . V O G K G . S V Y T A Q S D V O V P E N E S I K L T
SEQ ID NO: 2 45416 1 M G I L L G L L L G H L T Y D T Y G A P I L E V P E S V T G P W K G D V N L P

jam 49 C T Y S . . . G F S S P R V E W K F V Q G S T I A L V . . . C Y N S C I . T A P Y A D R V T F S .
45416 41 C T Y D P L O G Y T Q V L V K W L V Q R G S O P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H

jam 90 S S G I T F S S V T R K D N G E Y T C M Y . . . S E E G G O N Y G E V S I H L T Y L . V P P .
45416 91 K V P G D V S L A L S T I L E M D D O R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R A Y Q K L S V

jam 132 S K P T I S V P S . . . S V T I G N R A Y L T C S E H D G S P P S E Y S W F K D G I S H M L T A D A
45416 141 S K P T I V T T G S G Y G F T V P Q G W A I S L O C Q A R . G S P P I S Y I W Y K O O T N . . N Q E P

jam 178 K K T R A F W N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C O A Q N G Y C T A M R S E A A
45416 188 I K V A T L S T L L F K P A V I A D S G S Y F C T A K G O V G S E Q H S D I V

jam 228 H . . . M D A V E L N V G G I V A A V L V T I L G L L I F G . . . V W F A Y S R G Y F E T T K K
45416 227 K F V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K O S W D W T T D M D G Y L G E T S A

jam 272 G T A P G K K V I Y S Q P S T R S E G E F K O T S S F L V
45416 277 G P G X S L P V F A I I I S L C C M V V F I M A Y I M L C R K T S Q Q E H V Y E A A R

SEQ ID NO: 10	jam	1	W G T E G K A G R K L L F T S M I L G S L V O G K G S V Y T A o s D v o y . . . P E N E S I K L
SEQ ID NO: 29	35638	1	• • M A R R S R H R L L L R Y L V V A L G Y H X A Y G F S A P K C o a v t a v e y o e a i l
jam	48	T C . T Y S G F S S P R Y E W K F V Q G S I T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S	
35638	49	A C K T P K K T V S S R A L E W K K L . G R S V S F V Y Y Q Q T L Q G D F K N R A E M I D F N I R I K	
jam	97	S Y T R K D N G E Y T C M V S . . E E G G A N Y G E V S I H T V L V P P S K P T I S V P S S V T I	
35638	98	N Y T R A S D A G K Y R C E V S A P S E Q A N L E E D T V T L E V L V A P A V P S C E V P S S A L S	
jam	145	G N R A V Y L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F H N S S F T I D P K S	
35638	148	G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L . E N P R I G S Q S T N S S Y T W N T K T	
jam	195	G D L I F D P V T A F D S G E Y Y C O A Q N G Y G T A M A S E A A H W D A V E L N V G G I V A A V L	
35638	197	G T L O F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R M O V D D L N I S G I I A A V V	
jam	245	V T L I L L G L L I F G V W F A Y S R G Y F E T T K G T A P G K K V I Y S O P S T R S E G E F K Q	
35638	246	V V A L V I S V C C G L G V C Y A Q R K G Y F . . . S K E T S F O K S N S S S K A T I M S E N V Q O W L	
jam	295	T S S F L V	
35638	293	T P V I P A L W K A A A G G S R G Q E F	

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FIG..-17

SEQ ID NO: 6 A33_hum 1 M V G K M W P V L W T . L C A V R V T V D A I S V E T P Q D V L R A S O G K S V T L P C T
 SEQ ID NO: 10 jam 1 H G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L T C T

A33_hum 45 Y H T S T S S R E G L I Q W D K L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N N
 jam 51 Y S G F S S P R . . . V E W . X F V Q G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33_hum 95 A E Q S D A S I T I D Q L T W A D N G T Y E C S V S L W S D O L E G N T K S R V R L L V L V P P S K P
 jam 91 S G I T F S S V T R K D N G E Y T C M V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33_hum 145 E C G I E G E T I I G N N I Q L T C O S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S G Q
 jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D O G I S M I L T A D A K K T R A F M

A33_hum 195 P V S L K N I S T D T S G Y I C T S S N E E G T O F C N I T V A V R S P S H N . . . V A L
 jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A W R S E A A H M D A V E L

A33_hum 238 Y V . G I A V G V V A A L I I G I I Y C . . . C C C R G K D D N T E D K E D A R P N R E A Y E E
 jam 235 N V G G I V A A V L V T L I I L G L L I F G V W F A Y S R G Y F E . I T K K G T A P G K X V I Y S Q

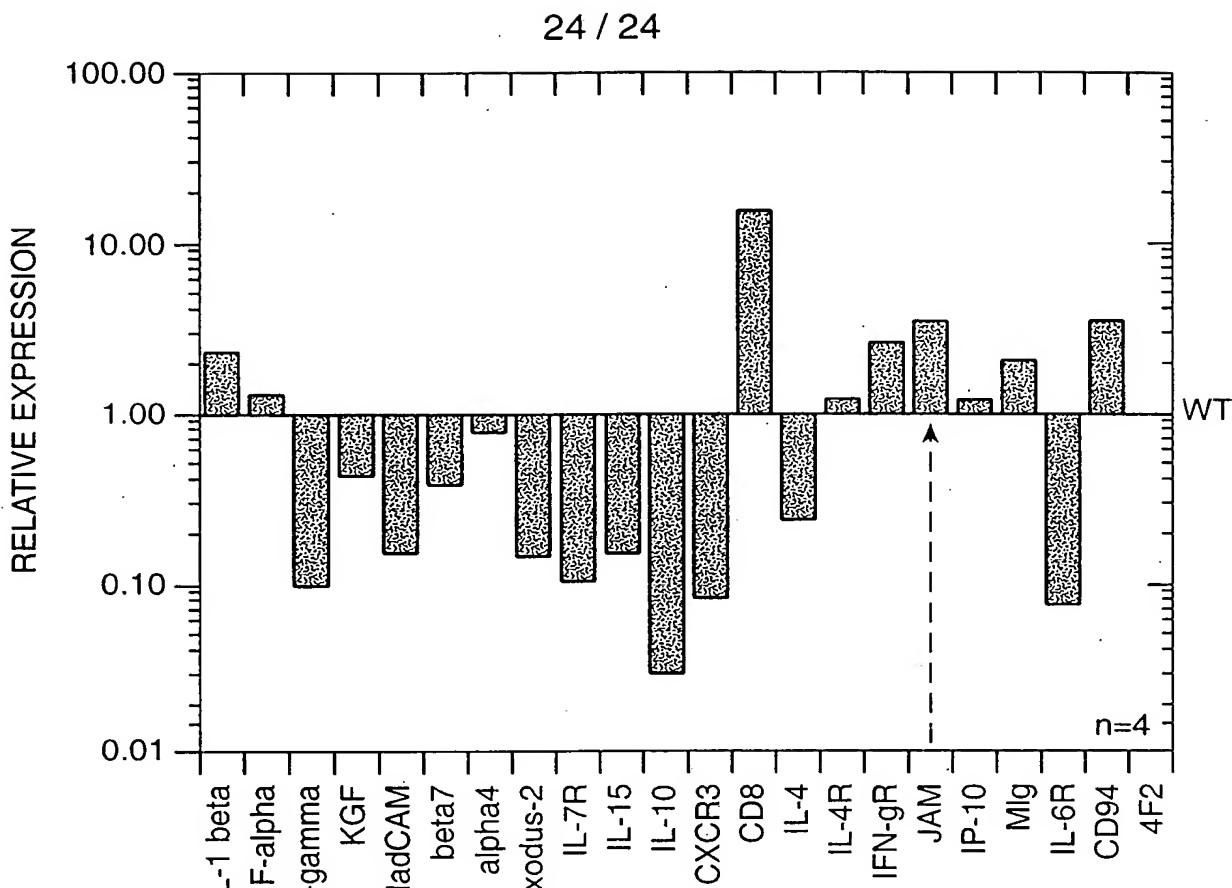
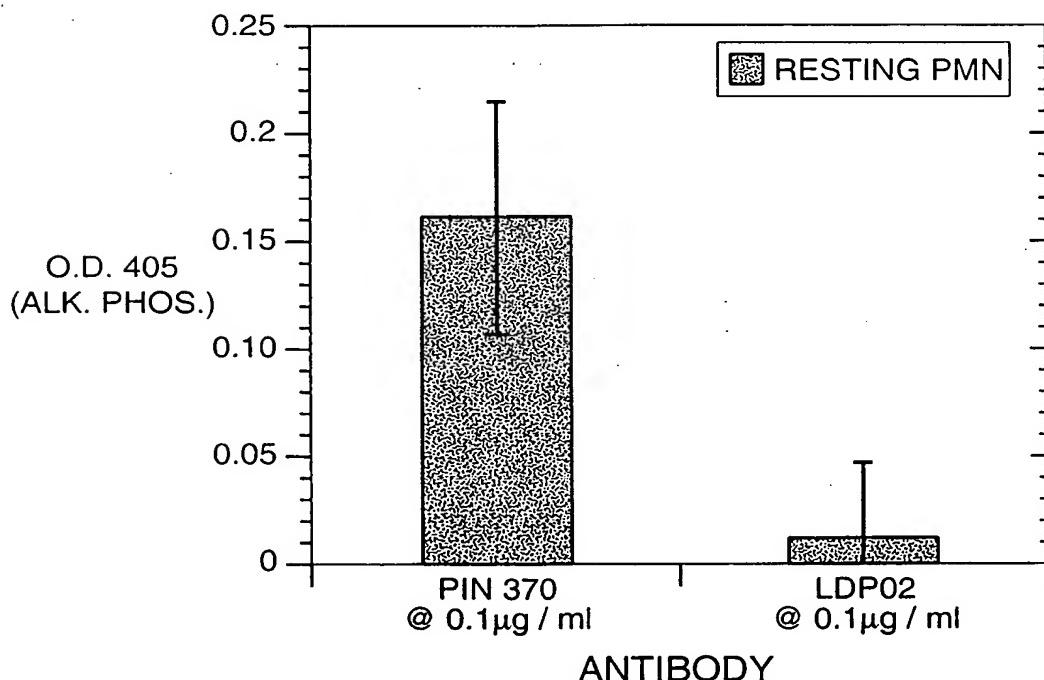
A33_hum 284 P P E Q L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D O
 jam 284 P S T R S E G E F K Q T S S F L V

FIG.._18

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++	APPENDIX	+
PUTAMEN	+	OVARY	++	LUNG	++++
SUSTANTIA NIGRA	+	PANCREAS	++	TRACHEA	+++
TEMPORAL LOBE	+	PITUITARY GLAND	++	PLACENTA	++++
THALAMUS	+	ADRENAL GLAND	++		
NUCLEUS ACCUMBENS	+	THYROID GLAND	++	FETAL BRAIN	+
SPINAL CORD	-	SALIVARY GLAND	++	FETAL HEART	+
		MAMMARY GLAND	++	FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	++++

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FIG.-19

**FIG._20****FIG._21**